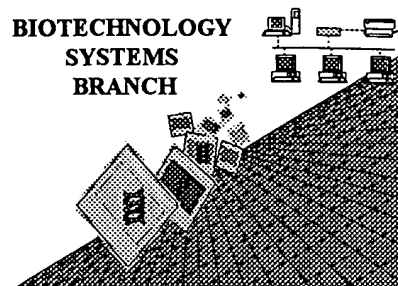


N. Johnson

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/833,506B
Art Unit / Team No. : 1642
Date Processed by STIC: 6/14/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

08/833,506B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506BDATE: 06/14/1999
TIME: 15:36:12

INPUT SET: S32213.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: ROBERT WEBBER
5 (ii) TITLE OF INVENTION: IMMUNOASSAY METHOD EMPLOYING MONOCLONAL
6 (iii) NUMBER OF SEQUENCES: 126
7 (iv) CORRESPONDENCE ADDRESS:
8 (A) ADDRESSEE: BIELEN, PETERSON & LAMPE
9 (B) STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720
10 (C) CITY: WALNUT CREEK
11 (D) STATE: CALIFORNIA
12 (E) COUNTRY: UNITED STATES OF AMERICA
13 (F) ZIP: 94596
14 (v) COMPUTER READABLE FORM:
15 (A) MEDIUM TYPE: DISKETTE 3.5 INCH, 1.44 MB FOR FORMATTED
16 (B) COMPUTER: IBM PC COMPATIBLE
17 (C) OPERATING SYSTEM: DOS
18 (D) SOFTWARE: WORDPERFECT 5.1
19 (vi) CURRENT APPLICATION DATA:
20 (A) APPLICATION NUMBER: NONE
21 (B) FILING DATE: NONE
22 (C) CLASSIFICATION:
23 (vii) PRIOR APPLICATION DATA:
24 (A) APPLICATION NUMBER: 08/634,332
25 (B) FILING DATE: 12 APRIL 1996
26 (viii) ATTORNEY/AGENT INFORMATION:
27 (A) NAME: THEODORE J. BIELEN, JR.
28 (B) REGISTRATION NUMBER: 27,420
29 (C) REFERENCE/DOCKET NUMBER: 12280
30 (ix) TELECOMMUNICATION INFORMATION:
31 (A) TELEPHONE: (925) 937-1515
32 (B) TELEFAX: (925) 937-1529
33
34

ANTIBODY REAC?

all text
must be
visible on
page

(see item 3
on Enov
summary
sheet)

-->

ERRORED SEQUENCES FOLLOW:

132 (2) INFORMATION FOR SEQ ID NO: 6:
133 (i) SEQUENCE CHARACTERISTICS:
134 (A) LENGTH: 17 18 shown
135 (B) TYPE: AMINO ACID
136 (D) TOPOLOGY: LINEAR

-->

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506BDATE: 06/14/1999
TIME: 15:36:12

INPUT SET: S32213.raw

137 (ii) MOLECULE TYPE: PEPTIDE
138 (ix) FEATURE:
139 (A) NAME/KEY: MOUSE iNOS (776-792)
140 (B) LOCATION:
141 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
142 (D) OTHER INFORMATION:
143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
144
145 Xaa Ala Leu Val Gln Gly Ile Leu Glu Arg Val Val Asp
146 1 5 5 10
147 Cys Pro Thr Pro His
148 15
149
150
151

(misaligned amino acids - see item 4
on Enr Summary Sheet)

152 (2) INFORMATION FOR SEQ ID NO: 7:
153 (i) SEQUENCE CHARACTERISTICS:
--> 154 (A) LENGTH: (15) 18 shown
155 (B) TYPE: AMINO ACID
156 (D) TOPOLOGY: LINEAR
157 (ii) MOLECULE TYPE: PEPTIDE
158 (ix) FEATURE:
159 (A) NAME/KEY: RAT iNOS (780-794)
160 (B) LOCATION:
161 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
162 (D) OTHER INFORMATION:
163 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
164
165 Xaa Xaa Leu Val Gln Gly Ile Leu Glu Arg Val Val Asp
166 5 10
167 Cys Ser Ser Pro Xaa
168 15
169
170

248 (2) INFORMATION FOR SEQ ID NO: 12:
249 (i) SEQUENCE CHARACTERISTICS:
--> 250 (A) LENGTH: (15) 18 shown
251 (B) TYPE: AMINO ACID
252 (D) TOPOLOGY: LINEAR
253 (ii) MOLECULE TYPE: PEPTIDE
254 (ix) FEATURE:
255 (A) NAME/KEY: HUMAN eNOS (1017-1031)
256 (B) LOCATION:
257 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
258 (D) OTHER INFORMATION:
259 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
260
261 Gly Ile Ala Pro Phe Arg Gly Phe Trp Gln Glu Arg Leu
262 5 10
263 His Asp Xaa Xaa Xaa
264 15

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506BDATE: 06/14/1999
TIME: 15:36:13

INPUT SET: S32213.raw

265
266

267 (2) INFORMATION FOR SEQ ID NO: 13:
268 (i) SEQUENCE CHARACTERISTICS:
--> 269 (A) LENGTH: (15) 18 show
270 (B) TYPE: AMINO ACID
271 (D) TOPOLOGY: LINEAR
272 (ii) MOLECULE TYPE: PEPTIDE
273 (ix) FEATURE:
274 (A) NAME/KEY: BOVINE eNOS (1019-1033)
275 (B) LOCATION:
276 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
277 (D) OTHER INFORMATION:
278 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
279
280 Gly Ile Ala Pro Phe Arg Gly Phe Trp Gln Glu Arg Leu
281 5 10
282 His Asp Xaa Xaa Xaa
283 15
284
285

1524 (2) INFORMATION FOR SEQ ID NO: 82:
--> OK 1525 (i) SEQUENCE CHARACTERISTICS:
1526 (A) LENGTH: 9
1527 (B) TYPE: AMINO ACID
1528 (D) TOPOLOGY: LINEAR
1529 (ii) MOLECULE TYPE: PEPTIDE
1530 (ix) FEATURE:
1531 (A) NAME/KEY: HUMAN iNOS (1009-1017)
1532 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1533 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1534 (D) OTHER INFORMATION:
1535 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:
1536
--> 1537 Arg Met Thr Leu Val Phe Gly Ser Arg-amide
1538 1 5
1539
1540

1541 (2) INFORMATION FOR SEQ ID NO: 83:
--> OK 1542 (i) SEQUENCE CHARACTERISTICS:
1543 (A) LENGTH: 6
1544 (B) TYPE: AMINO ACID
1545 (D) TOPOLOGY: LINEAR
1546 (ii) MOLECULE TYPE: PEPTIDE
1547 (ix) FEATURE:
1548 (A) NAME/KEY: HUMAN iNOS (1009-1014)
1549 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
1550 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
1551 (D) OTHER INFORMATION:
1552 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

delete - do not show this
in the sequence
itself

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/833,506BDATE: 06/14/1999
TIME: 15:36:13

INPUT SET: S32213.raw

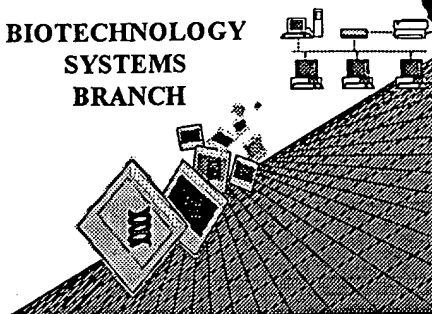
--> 1553
1554 Arg Met Thr Leu Val Phe-amide *delete*
1555 1
1556
1557
1558

2296 (2) INFORMATION FOR SEQ ID NO: 126:
2297 (i) SEQUENCE CHARACTERISTICS:
2298 (A) LENGTH: 8
2299 (B) TYPE: AMINO ACID
2300 (D) TOPOLOGY: LINEAR
2301 (ii) MOLECULE TYPE: PEPTIDE
2302 (ix) FEATURE:
2303 (A) NAME/KEY: HUMAN iNOS (783-790)
2304 (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
2305 (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
2306 (D) OTHER INFORMATION:
2307
2308 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:
2309
2310 Leu Val Gln Gly Ile Leu Glu Arg
2311 5
--> 2312 *??*
2313 *delete at*
2314 *end of file*
2315
2316
2317
2318
2319
2320
2321
2322
2323
2324
2325

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/833,506BDATE: 06/14/1999
TIME: 15:36:13**INPUT SET: S32213.raw**

Line	Error	Original Text
20	Wrong application Serial Number	(A) APPLICATION NUMBER: NONE
134	Entered (17) and Calc. Seq. Length (18) differ	(A) LENGTH: 17
154	Entered (15) and Calc. Seq. Length (18) differ	(A) LENGTH: 15
250	Entered (15) and Calc. Seq. Length (18) differ	(A) LENGTH: 15
269	Entered (15) and Calc. Seq. Length (18) differ	(A) LENGTH: 15
1526	Entered (9) and Calc. Seq. Length (8) differ	(A) LENGTH: 9
1537	Wrong Amino Acid Designator	Arg Met Thr Leu Val Phe Gly Ser Arg-amide
1543	Entered (6) and Calc. Seq. Length (5) differ	(A) LENGTH: 6
1554	Wrong Amino Acid Designator	Arg Met Thr Leu Val Phe-amide
2312	Wrong Amino Acid Designator	??

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Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825). Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: `pub/checker/`
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
WASHINGTON DC 20231

COST FOR DISKETTE IS \$ 25.00

METHOD OF PAYMENT:

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VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737
PTO Deposit Account

*For Further Information, Contact: **Arti Shah at 703-308-4212***